

SEQUENCE LISTING

<110> Magna, Holly
 Schaffer, Paul
 Lawton, Michael
 Yocum, Sue
 Mitchell, Peter
 Hutchinson, Nancy
 Murry, Lynn E.

<120> HUMAN NUCLEOTIDE PYROPHOSPHOHYDROLASE-2

<130> PF-0420 US

<140> 08/996,083

<141> 1997-12-22

<160> 3

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1156

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No.: 1388013

<300>

<400> 1

Met	Ala	Ser	Leu	Leu	Pro	Leu	Leu	Cys	Leu	Cys	Val	Val	Ala	Ala	His
1				5					10					15	
Leu	Ala	Gly	Ala	Arg	Asp	Ala	Thr	Pro	Thr	Glu	Glu	Pro	Met	Ala	Thr
			20					25					30		
Ala	Leu	Gly	Leu	Glu	Arg	Arg	Ser	Val	Tyr	Thr	Gly	Gln	Pro	Ser	Pro
		35					40					45			
Ala	Leu	Glu	Asp	Trp	Glu	Glu	Ala	Ser	Glu	Trp	Thr	Ser	Trp	Phe	Asn
	50					55				60					
Val	Asp	His	Pro	Gly	Gly	Asp	Gly	Asp	Phe	Glu	Ser	Leu	Ala	Ala	Ile
65					70					75					80
Arg	Phe	Tyr	Tyr	Gly	Pro	Ala	Arg	Val	Cys	Pro	Arg	Pro	Leu	Ala	Leu
			85					90					95		
Glu	Ala	Arg	Thr	Thr	Asp	Trp	Ala	Leu	Pro	Ser	Ala	Val	Gly	Glu	Arg
			100					105					110		
Val	His	Leu	Asn	Pro	Thr	Arg	Gly	Phe	Trp	Cys	Leu	Asn	Arg	Glu	Gln
		115					120					125			
Pro	Arg	Gly	Arg	Arg	Cys	Ser	Asn	Tyr	His	Val	Arg	Phe	Arg	Cys	Pro
	130					135					140				
Leu	Glu	Ala	Ser	Trp	Gly	Ala	Trp	Gly	Pro	Trp	Gly	Pro	Cys	Ser	Gly
145					150					155					160
Ser	Cys	Gly	Pro	Gly	Arg	Arg	Leu	Arg	Arg	Arg	His	Cys	Pro	Ser	Pro
			165					170						175	
Ala	Gly	Asp	Ala	Cys	Pro	Gly	Arg	Pro	Leu	Glu	Ala	Gln	Lys	Cys	Val
		180						185					190		
Arg	Pro	Arg	Cys	Pro	Gly	Cys	Ser	Leu	Asp	Thr	Cys	Glu	Cys	Pro	Asp
		195					200					205			
His	Ile	Leu	Leu	Gly	Ser	Val	Val	Thr	Pro	Ser	Gly	Gln	Pro	Leu	Leu

210	215	220
Gly Ala Arg Val Ser	Leu Arg Asp Gln Pro	Gly Thr Val Ala Thr Ser
225	230	235
Asp Ala His Gly Thr	Phe Arg Val Pro	Gly Val Cys Ala Asp Ser Arg
245	250	255
Ala Asn Ile Arg	Ala Gln Met Asp	Gly Phe Ser Ala Gly Glu Ala Gln
260	265	270
Ala Gln Ala Asn Gly	Ser Ile Ser Val	Val Thr Ile Ile Leu Asp Lys
275	280	285
Leu Glu Lys Pro Tyr	Leu Val Lys His	Pro Glu Ser Arg Val Arg Glu
290	295	300
Ala Gly Gln Asn Val	Thr Phe Cys Cys Lys	Ala Ser Gly Thr Pro Met
305	310	315
Pro Lys Lys Tyr Ser	Trp Phe His Asn Gly	Thr Leu Leu Asp Arg Arg
325	330	335
Ala His Gly Tyr Gly	Ala His Leu Glu	Leu Arg Gly Leu Arg Pro Asp
340	345	350
Gln Ala Gly Ile Tyr	His Cys Lys Ala	Trp Asn Glu Ala Gly Ala Val
355	360	365
Arg Ser Gly Thr Ala	Arg Leu Thr Val	Leu Ala Pro Gly Gln Pro Ala
370	375	380
Cys Asp Pro Arg Pro	Arg Glu Tyr Leu	Ile Lys Leu Pro Glu Asp Cys
385	390	395
Gly Gln Pro Gly Ser	Gly Pro Ala Tyr	Leu Asp Val Gly Leu Cys Pro
405	410	415
Asp Thr Arg Cys Pro	Ser Leu Ala Gly	Ser Ser Pro Arg Cys Gly Asp
420	425	430
Ala Ser Ser Arg Cys	Cys Ser Val Arg	Arg Arg Leu Glu Arg Arg Glu Ile
435	440	445
His Cys Pro Gly Tyr	Val Leu Pro Val	Lys Val Val Ala Glu Cys Gly
450	455	460
Cys Gln Lys Cys Leu	Pro Pro Arg Gly	Leu Val Arg Gly Arg Val Val
465	470	475
Ala Ala Asp Ser Gly	Glu Pro Leu Arg	Phe Ala Arg Ile Leu Leu Gly
485	490	495
Gln Glu Pro Ile Gly	Phe Thr Ala Tyr	Gln Gly Asp Phe Thr Ile Glu
500	505	510
Val Pro Pro Ser Thr	Gln Arg Leu Val	Val Thr Phe Val Asp Pro Ser
515	520	525
Gly Glu Phe Met Asp	Ala Val Arg Val	Leu Pro Phe Asp Pro Arg Gly
530	535	540
Ala Gly Val Tyr His	Glu Val Lys Ala	Met Arg Lys Lys Ala Pro Val
545	550	555
Ile Leu His Thr Ser	Gln Ser Asn Thr	Ile Pro Leu Gly Glu Leu Glu
565	570	575
Asp Glu Ala Pro Leu	Gly Glu Leu Val	Leu Pro Ser Gly Ala Phe Arg
580	585	590
Arg Ala Asp Gly Lys	Pro Tyr Ser Gly	Pro Val Glu Ala Arg Val Thr
595	600	605
Phe Val Asp Pro Arg	Asp Leu Thr Ser	Ala Ala Ser Ala Pro Ser Asp
610	615	620
Leu Arg Phe Val Asp	Ser Asp Gly Glu	Leu Ala Pro Leu Arg Thr Tyr
625	630	635
Gly Met Phe Ser Val	Asp Leu Arg Ala	Pro Gly Ser Ala Glu Gln Leu
645	650	655
Gln Val Gly Pro Val	Ala Val Arg Val	Ala Ala Ser Gln Ile His Met
660	665	670
Pro Gly His Val Glu	Ala Leu Lys Leu	Trp Ser Leu Asn Pro Glu Thr
675	680	685
Gly Leu Trp Glu Glu	Glu Ser Gly Phe	Arg Arg Glu Gly Ser Ser Gly
690	695	700

PF-0420 US

```

Pro Arg Val Arg Arg Glu Glu Arg Val Phe Leu Val Gly Asn Val Glu
705          710          715          720
Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Arg Arg Arg
          725          730          735
Cys Phe Val Lys Val Arg Ala Tyr Ala Asn Asp Lys Phe Thr Pro Ser
          740          745          750
Glu Gln Val Glu Gly Val Val Val Thr Leu Val Asn Leu Glu Pro Ala
          755          760          765
Pro Gly Phe Ser Ala Asn Pro Arg Ala Trp Gly Arg Phe Asp Ser Ala
          770          775          780
Val Thr Gly Pro Asn Gly Ala Cys Leu Pro Ala Phe Cys Asp Ala Asp
785          790          795          800
Arg Pro Asp Ala Tyr Thr Ala Leu Val Thr Ala Thr Leu Gly Gly Glu
          805          810          815
Glu Leu Glu Pro Ala Pro Ser Leu Pro Arg Pro Leu Pro Ala Thr Val
          820          825          830
Gly Val Thr Gln Pro Tyr Leu Asp Arg Leu Gly Tyr Arg Arg Thr Asp
          835          840          845
His Asp Asp Pro Ala Phe Lys Arg Asn Gly Phe Arg Ile Asn Leu Ala
          850          855          860
Lys Pro Arg Pro Gly Asp Pro Ala Glu Ala Asn Gly Pro Val Tyr Pro
865          870          875          880
Trp Arg Ser Leu Arg Glu Cys Gln Gly Ala Pro Val Thr Ala Ser His
          885          890          895
Phe Arg Phe Ala Arg Val Glu Ala Asp Lys Tyr Glu Tyr Asn Val Val
          900          905          910
Pro Phe Arg Glu Gly Thr Pro Ala Ser Trp Thr Gly Asp Leu Leu Ala
          915          920          925
Trp Trp Pro Asn Pro Gln Glu Phe Arg Ala Cys Phe Leu Lys Val Lys
930          935          940
Ile Gln Gly Pro Gln Glu Tyr Met Val Arg Ser His Asn Ala Gly Gly
945          950          955          960
Ser His Pro Arg Thr Arg Gly Gln Leu Tyr Gly Leu Arg Asp Ala Arg
          965          970          975
Ser Val Arg Asp Pro Glu Arg Pro Gly Thr Ser Ala Ala Cys Val Glu
          980          985          990
Phe Lys Cys Ser Gly Met Leu Phe Asp Gln Arg Gln Val Asp Arg Thr
          995          1000          1005
Leu Val Thr Ile Met Pro Gln Gly Ser Cys Arg Arg Val Ala Val Asn
1010          1015          1020
Gly Leu Leu Arg Asp Tyr Leu Thr Arg His Pro Pro Pro Val Pro Ala
1025          1030          1035          1040
Glu Asp Pro Ala Ala Phe Ser Met Leu Ala Pro Leu Asp Pro Leu Gly
          1045          1050          1055
His Asn Tyr Gly Val Tyr Thr Val Thr Asp Gln Ser Pro Arg Leu Ala
          1060          1065          1070
Lys Glu Ile Ala Ile Gly Arg Cys Phe Asp Gly Ser Ser Asp Gly Phe
          1075          1080          1085
Ser Arg Glu Met Lys Ala Asp Ala Gly Thr Ala Val Thr Phe Gln Cys
1090          1095          1100
Arg Glu Pro Pro Ala Gly Arg Pro Ser Leu Phe Gln Arg Leu Leu Glu
1105          1110          1115          1120
Ser Pro Ala Thr Ala Leu Gly Asp Ile Arg Arg Glu Met Ser Glu Ala
          1125          1130          1135
Ala Gln Ala Gln Ala Arg Ala Ser Gly Pro Leu Arg Thr Arg Arg Gly
          1140          1145          1150
Arg Val Arg Gln
          1155

```

<210> 2

PF-0420 US

<211> 4183

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No.: 1388013

<300>

<400> 2

gccccgagcac	gccgcggagc	cgggacctcc	ctcggacgct	ctgccccggc	catggcgctc	60
ctgctgccac	tgtctgtct	ctgtgtcgtc	gctgcgcacc	tggcgggggc	cggagacgcc	120
acccccaccg	aggagccaat	ggcgactgca	ctgggccttg	aaagacggtc	cgtgtacacc	180
ggccagccct	caccagccct	ggaggactgg	gaagaggcca	gcgagtggac	gtcctgggtc	240
aacgtggacc	accccgagg	cgacggcgac	ttcgagagcc	tggctgccat	cgccttctac	300
tacggggccag	cgcgcgtgtg	cccgcgaccg	ctggcgctgg	aggcgcgcac	cacggactgg	360
gccctgccgt	ccgccgtcgg	cgagcgcggtg	cacttgaacc	ccacgcgcgg	cttctgggtc	420
ctcaaccgcg	agcaaccgcg	tggccgcgcg	tgtccaact	accacgtgcg	cttccgctgc	480
ccactagaag	cctcgtgggg	cgcgtggggc	ccgtggggtc	cctgctcggg	gagctgtggg	540
ccaggccgtc	gcttgcgcgg	ccgccactgc	ccaagccccc	ctgggggatgc	gtgtcccggg	600
cgtcctctgg	aggcgagaaa	gtgcgtgcgg	cctcgggtgtc	cagggtgcag	ccttgacacc	660
tgtgaatgcc	cggaccacat	cctcctgggc	tcgggtgtca	ccccatctgg	gcaaccactg	720
ctaggagcca	gggtctccct	gcgagaccag	cctggcactg	tggccaaccg	cgatgctcac	780
ggaaccttcc	gggtgcctgg	tgtctgtgct	gacagccgcg	ccaacatcag	ggcccagatg	840
gatggcttct	ctgcagggga	ggcccaggcc	caggccaacg	gatccatctc	tgtggtcacc	900
atcatccttg	ataagtggga	gaagccgtac	ctgggtgaaac	accctgagtc	ccgagtgcga	960
gaggctggcc	agaatgtgac	tttctgctgc	aaagcctccg	ggacccccat	gcccagaata	1020
tactcctggt	tccacaatgg	gacctgtctg	gacaggcgag	ctcatgggta	cggggccccc	1080
ctggagctsc	ggggactgcg	cccagaccag	gctggcatct	accactgcaa	ggcatggaat	1140
gaggcgggtg	ccgtgcgctc	gggcactgcc	cggtcactg	tacttgcccc	aggccagcca	1200
gcctgcagcc	cccggccccc	agagtacctg	atcaagctcc	ctgaggactg	tggtcagcca	1260
ggtagtgccc	ctgcctacct	ggatgtgggg	ctctgtcccc	acaccgctg	ccccagcctg	1320
gcaggctcca	gcccccgctg	cgggggacgc	agctcccgc	gctgctctgt	gcgcgcgtct	1380
gagagaaggg	agattcactg	ccctggctac	gtcctcccag	tgaagggtgg	ggcagagtgt	1440
ggctgccaga	agtgtctgcc	ccctcggggg	ctggctccgg	gccgtgttgt	ggctgctgac	1500
tccggggagc	cgtacgctt	cgccaggatt	ctgctgggcc	aggagcccat	cggcttcacc	1560
gcctaccagg	gcgactttac	cattgaggtg	ccgcctcca	cccagcggct	ggtgggtgact	1620
tttgtggacc	ccagcgggtg	gttcatggac	gctgtccggg	tcttgccctt	tgatcctcga	1680
ggtgccggcg	tgtaccacga	ggtcaaggcc	atgcggaaga	aagccccgg	cattttacat	1740
accagccaga	gcaacacgat	ccccctgggc	gagctggaag	atgaggcgcc	cctgggcgag	1800
ctggctcctg	cttctggcgc	tttccgcaga	gccgacggca	aacctactc	ggggcctgtg	1860
gaggccccgg	tgacgttcgt	ggacccccga	gacctcacct	cggcggcgct	tgccccagtc	1920
gacctgcgct	tcgtggacag	cgacggcgag	ctggtccac	tgcgcaccta	cggcatgttc	1980
tccgtggacc	tccgtgcgcc	cggctccgcg	gagcagctgc	aggtggggcc	ggtggccgtg	2040
cgggtggccg	ccagccagat	ccacatgcca	ggccacgtgg	aggccctcaa	gctgtgggtc	2100
ctgaaccccc	agaccggctt	gtgggaggag	gagagcggct	tccggcgcca	ggggctctcg	2160
ggcccccggg	tgcgcgggga	ggagcgcgtc	ttcctggtgg	gcaacgtgga	gatccgggag	2220
cggcgccgtg	tcaatctgga	cgtgcctgag	cgcgcctgct	gcttcgtgaa	ggtgcgcgcc	2280
tacgccaaac	acaagtccac	ccccagcgag	caggtggagg	gcgtgggtgg	cacgctgggt	2340
aatctggagc	cgcccccgg	cttctccgcc	aacccccgtg	cctggggccg	ctttgacagc	2400
gcggctaccg	gccccaatgg	cgcctgcctc	ccgccttct	gcgacgccga	caggccagac	2460
gcctacaccg	ccctggtcac	cgcacacctg	ggcggcgagg	agctggagcc	ggccccctcc	2520
ttgccccgcc	cactcccgcc	caccgtgggc	gtcaccagc	cctacctgga	caggctgggg	2580
taccgtcgga	cggaccacga	cgatcccgcc	ttcaagcgta	acggcttccg	catcaacctc	2640
gccaagccca	ggccagggtg	ccccgcggag	gccaatgggc	ctgtgtaccc	gtggcgagc	2700
ctgcgggaat	gccagggggc	cccgggtgact	gccagccact	tccgcttcgc	cagggtggag	2760
gcggacaagt	acgagtacaa	cgtgggtccc	ttccgagagg	gcacacctgc	ctcctggact	2820
ggcgatctcc	tggcctggtg	gccccaaccc	caggagttcc	gggcctgctt	cctcaagggt	2880
aagatccagg	gtccccagga	gtatatgggt	cgtccccaca	acgcaggggg	cagccaccca	2940
cgcacccgcg	gccagctcta	cggacttcgg	gatgcccgga	gtgtgcgaga	ccccgagcgt	3000

```

ccggggcacct cggcagcctg cgtggagttc aagtgcagcg ggatgctgtt cgaccagcgg 3060
caggtgggaca ggacgctggg gaccattatg ccccagggca gctgccggcg cgtggccgctc 3120
aacgggactcc ttcgggatta cctgacccgg cacccccac cgtgcccgc ggaggacca 3180
gctgoccttct ccatgctggc cccctagac cctctggggc acaactatgg cgtctacact 3240
gtcactgacc agagcccacg cttggccaag gagatcgcca ttggccgctg ctttgatggg 3300
tcctctgacg gytctctccag agagatgaag gctgatgccg gcacagccgt caccttccag 3360
tgccggggagc caccggccgg acgacccagc ctcttccaga ggctgctgga gtccccggcg 3420
acagcacttg gtgacatccg cagggagatg agcgaggcgg cgcaggcaca ggcccggggc 3480
tcaggtcccc tccgcacccg ccggggtagg gtccggcagt gacctgggca ggggcctcgc 3540
tttcccacct cctccagac tcctttgacc ccaggaagtt ttgcccctcc ttcttctcca 3600
gacagcccc tccccaggtg tctgggtccc ctttcccggc cctttccaga actcagagtc 3660
agacaagaac ccagagcatc cgatggtaga aacaccagga agacaattgt tgctgtgtgg 3720
tatggaatgg agtttgcggt gactctgggg ccagcaccca ggggacgacg ttcaacccta 3780
gctgaagggg acccgctccc agctcagaag ccgtctctga cttctcgtgc gtattttgac 3840
cctgatttca atcttctacc cttgggagtt ctggcgtttg gcacaaagtc cctctgcct 3900
gtttggagct cagtgtctga ccaggtcccc tgccccgagc tttgtttttg gggttattta 3960
ttgaaacaaa gtgtggggag ctggttgtgg gtgtgagtgg ggggtgtggg tccaggtgg 4020
gcccagtgaa aaggaggaag gggttcccat gcgggggagg ctctggggct gaggggaaca 4080
attctcacgt gtttggtgct tagagacctg cccggggcgt tgggcaggcc ctccgggggc 4140
tgaattaaaa atgctttatt tcaaaaaaaa aaaaaaaaaa aaa 4183

```

<210> 3

<211> 1184

<212> PRT

<213> Homo sapiens

<220>

<221>misc_feature

<223>Incyte Clone No.: 422069

<300>

<400> 3

```

Met Val Gly Thr Lys Ala Trp Val Phe Ser Phe Leu Val Leu Glu Val
1          5          10          15
Thr Ser Val Leu Gly Arg Gln Thr Met Leu Thr Gln Ser Val Arg Arg
20          25          30
Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys Pro Ala Asp
35          40          45
Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe Asn Ile Asp Tyr
50          55          60
Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp Ala Ile Arg Phe Tyr
65          70          75          80
Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu Arg Leu Glu Ala Arg Thr
85          90          95
Thr Asp Trp Thr Pro Ala Gly Ser Thr Gly Gln Val Val His Gly Ser
100         105         110
Pro Arg Glu Gly Phe Trp Cys Leu Asn Arg Glu Gln Arg Pro Gly Gln
115         120         125
Asn Cys Ser Asn Tyr Thr Val Arg Phe Leu Cys Pro Pro Gly Ser Leu
130         135         140
Arg Arg Asp Thr Glu Arg Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys
145         150         155         160
Cys Ser Ala Ala Cys Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile
165         170         175
Cys Leu Ala Glu Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly
180         185         190
Gln His Cys Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro
195         200         205
Met Gly Gln Val Asn Ala Asp Cys Asp Ala Cys Met Cys Gln Asp Phe
210         215         220

```

PF-0420 US

Met	Leu	His	Gly	Ala	Val	Ser	Leu	Pro	Gly	Gly	Ala	Pro	Ala	Ser	Gly
225					230					235					240
Ala	Ala	Ile	Tyr	Leu	Leu	Thr	Lys	Thr	Pro	Lys	Leu	Leu	Thr	Gln	Thr
				245					250					255	
Asp	Ser	Asp	Gly	Arg	Phe	Arg	Ile	Pro	Gly	Leu	Cys	Pro	Asp	Gly	Lys
			260					265					270		
Ser	Ile	Leu	Lys	Ile	Thr	Lys	Val	Lys	Phe	Ala	Pro	Ile	Val	Leu	Thr
		275					280					285			
Met	Pro	Lys	Thr	Ser	Leu	Lys	Ala	Ala	Thr	Ile	Lys	Ala	Glu	Phe	Val
	290					295					300				
Arg	Ala	Glu	Thr	Pro	Tyr	Met	Val	Met	Asn	Pro	Glu	Thr	Lys	Ala	Arg
305					310				315						320
Arg	Ala	Gly	Gln	Ser	Val	Ser	Leu	Cys	Cys	Lys	Ala	Thr	Gly	Lys	Pro
			325						330					335	
Arg	Pro	Asp	Lys	Tyr	Phe	Trp	Tyr	His	Asn	Asp	Thr	Leu	Leu	Asp	Pro
			340					345					350		
Ser	Leu	Tyr	Lys	His	Glu	Ser	Lys	Leu	Val	Leu	Arg	Lys	Leu	Gln	Gln
		355					360					365			
His	Gln	Ala	Gly	Glu	Tyr	Phe	Cys	Lys	Ala	Gln	Ser	Asp	Ala	Gly	Ala
	370					375				380					
Val	Lys	Ser	Lys	Val	Ala	Gln	Leu	Ile	Val	Ile	Ala	Ser	Asp	Glu	Thr
385					390				395						400
Pro	Cys	Asn	Pro	Val	Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Leu	Pro	His	Asp
				405					410					415	
Cys	Phe	Gln	Asn	Ala	Thr	Asn	Ser	Phe	Tyr	Tyr	Asp	Val	Gly	Arg	Cys
			420					425					430		
Pro	Val	Lys	Thr	Cys	Ala	Gly	Gln	Gln	Asp	Asn	Gly	Ile	Arg	Cys	Arg
		435					440					445			
Asp	Ala	Val	Gln	Asn	Cys	Cys	Gly	Ile	Ser	Lys	Thr	Glu	Glu	Arg	Glu
	450					455					460				
Ile	Gln	Cys	Ser	Gly	Tyr	Thr	Leu	Pro	Thr	Lys	Val	Ala	Lys	Glu	Cys
465					470					475					480
Ser	Cys	Gln	Arg	Cys	Thr	Glu	Thr	Arg	Ser	Ile	Val	Arg	Gly	Arg	Val
				485					490					495	
Ser	Ala	Ala	Asp	Asn	Gly	Glu	Pro	Met	Arg	Phe	Gly	His	Val	Tyr	Met
			500					505					510		
Gly	Asn	Ser	Arg	Val	Ser	Met	Thr	Gly	Tyr	Lys	Gly	Thr	Phe	Thr	Leu
		515					520					525			
His	Val	Pro	Gln	Asp	Thr	Glu	Arg	Leu	Val	Leu	Thr	Phe	Val	Asp	Arg
	530					535					540				
Leu	Gln	Lys	Phe	Val	Asn	Thr	Thr	Lys	Val	Leu	Pro	Phe	Asn	Lys	Lys
545					550					555					560
Gly	Ser	Ala	Val	Phe	His	Glu	Ile	Lys	Met	Leu	Cys	Arg	Lys	Glu	Pro
				565					570					575	
Ile	Thr	Leu	Glu	Ala	Met	Glu	Thr	Asn	Ile	Ile	Pro	Leu	Gly	Glu	Val
			580					585					590		
Val	Gly	Glu	Asp	Pro	Met	Ala	Glu	Leu	Glu	Ile	Pro	Ser	Arg	Ser	Phe
		595					600					605			
Tyr	Arg	Gln	Asn	Gly	Glu	Pro	Tyr	Ile	Gly	Lys	Val	Lys	Ala	Ser	Val
	610					615					620				
Thr	Phe	Leu	Asp	Pro	Arg	Asn	Ile	Ser	Thr	Ala	Thr	Ala	Ala	Gln	Thr
625					630					635					640
Asp	Leu	Asn	Phe	Ile	Asn	Asp	Glu	Gly	Asp	Thr	Phe	Pro	Leu	Arg	Thr
				645					650					655	
Tyr	Gly	Met	Phe	Ser	Val	Asp	Phe	Arg	Asp	Glu	Val	Thr	Ser	Glu	Pro
			660					665					670		
Leu	Asn	Ala	Gly	Lys	Val	Lys	Val	His	Leu	Asp	Ser	Thr	Gln	Val	Lys
		675					680					685			
Met	Pro	Glu	His	Ile	Ser	Thr	Val	Lys	Leu	Trp	Ser	Leu	Asn	Pro	Asp
	690					695						700			

PF-0420 US

Thr	Gly	Leu	Trp	Glu	Glu	Glu	Gly	Asp	Phe	Lys	Phe	Glu	Asn	Gln	Arg
705					710					715					720
Arg	Asn	Lys	Arg	Glu	Asp	Arg	Thr	Phe	Leu	Val	Gly	Asn	Leu	Glu	Ile
				725					730					735	
Arg	Glu	Arg	Arg	Leu	Phe	Asn	Leu	Asp	Val	Pro	Glu	Ser	Arg	Arg	Cys
				740				745					750		
Phe	Val	Lys	Val	Arg	Ala	Tyr	Arg	Ser	Glu	Arg	Phe	Leu	Pro	Ser	Glu
		755					760					765			
Gln	Ile	Gln	Gly	Val	Val	Ile	Ser	Val	Ile	Asn	Leu	Glu	Pro	Arg	Thr
	770					775					780				
Gly	Phe	Leu	Ser	Asn	Pro	Arg	Ala	Trp	Gly	Arg	Phe	Asp	Ser	Val	Ile
785					790					795					800
Thr	Gly	Pro	Asn	Gly	Ala	Cys	Val	Pro	Ala	Phe	Cys	Asp	Asp	Gln	Ser
				805					810					815	
Pro	Asp	Ala	Tyr	Ser	Ala	Tyr	Val	Leu	Ala	Ser	Leu	Ala	Gly	Glu	Glu
				820				825					830		
Leu	Gln	Ala	Val	Glu	Ser	Ser	Pro	Lys	Phe	Asn	Pro	Asn	Ala	Ile	Gly
		835					840					845			
Val	Pro	Gln	Pro	Tyr	Leu	Asn	Lys	Leu	Asn	Tyr	Arg	Arg	Thr	Asp	His
	850					855					860				
Glu	Asp	Pro	Arg	Val	Lys	Lys	Thr	Ala	Phe	Gln	Ile	Ser	Met	Ala	Lys
865					870					875					880
Pro	Arg	Pro	Asn	Ser	Ala	Glu	Glu	Ser	Asn	Gly	Pro	Ile	Tyr	Ala	Phe
				885					890					895	
Glu	Asn	Leu	Arg	Ala	Cys	Glu	Glu	Ala	Pro	Pro	Ser	Ala	Ala	His	Phe
				900				905					910		
Arg	Phe	Tyr	Gln	Ile	Glu	Gly	Asp	Arg	Tyr	Asp	Tyr	Asn	Thr	Val	Pro
		915					920					925			
Phe	Asn	Glu	Asp	Asp	Pro	Met	Ser	Trp	Thr	Glu	Asp	Tyr	Leu	Ala	Trp
	930					935					940				
Trp	Pro	Lys	Pro	Met	Glu	Phe	Arg	Ala	Cys	Tyr	Ile	Lys	Val	Lys	Ile
945					950					955					960
Val	Gly	Pro	Leu	Glu	Val	Asn	Val	Arg	Ser	Arg	Asn	Met	Gly	Gly	Thr
				965					970					975	
His	Arg	Arg	Thr	Val	Gly	Lys	Leu	Tyr	Gly	Ile	Arg	Asp	Val	Arg	Ser
			980					985					990		
Thr	Arg	Asp	Arg	Asp	Gln	Pro	Asn	Val	Ser	Ala	Ala	Cys	Leu	Glu	Phe
		995					1000					1005			
Lys	Cys	Ser	Gly	Met	Leu	Tyr	Asp	Gln	Asp	Arg	Val	Asp	Arg	Thr	Leu
	1010					1015					1020				
Val	Lys	Val	Ile	Pro	Gln	Gly	Ser	Cys	Arg	Arg	Ala	Ser	Val	Asn	Pro
1025					1030					1035					1040
Met	Leu	His	Glu	Tyr	Leu	Val	Asn	His	Leu	Pro	Leu	Ala	Val	Asn	Asn
				1045					1050					1055	
Asp	Thr	Ser	Glu	Tyr	Thr	Met	Leu	Ala	Pro	Leu	Asp	Pro	Leu	Gly	His
			1060					1065					1070		
Asn	Tyr	Gly	Ile	Tyr	Thr	Val	Thr	Asp	Gln	Asp	Pro	Arg	Thr	Ala	Lys
	1075						1080					1085			
Glu	Ile	Ala	Leu	Gly	Arg	Cys	Phe	Asp	Gly	Thr	Ser	Asp	Gly	Ser	Ser
	1090					1095					1100				
Arg	Ile	Met	Lys	Ser	Asn	Val	Gly	Val	Ala	Leu	Thr	Phe	Asn	Cys	Val
1105					1110					1115					1120
Glu	Arg	Gln	Val	Gly	Arg	Gln	Ser	Ala	Phe	Gln	Tyr	Leu	Gln	Ser	Thr
				1125					1130					1135	
Pro	Ala	Gln	Ser	Pro	Ala	Ala	Gly	Thr	Val	Gln	Gly	Arg	Val	Pro	Ser
			1140					1145					1150		
Arg	Arg	Gln	Gln	Arg	Ala	Ser	Arg	Gly	Gly	Gln	Arg	Gln	Ser	Gly	Val
		1155					1160					1165			
Val	Ala	Ser	Leu	Arg	Phe	Pro	Arg	Val	Ala	Gln	Gln	Pro	Leu	Ile	Asn
	1170					1175					1180				